Amendments to the Claims:

1-22. (Cancelled)

23. (Withdrawn) A method of ordering pairs of sequence tags, the method comprising the steps of:

a) providing a population of pairs of sequence tags of restriction fragments, produced by digesting a fragment of genomic DNA with a plurality of combinations of restriction endonucleases;

b) removing duplicate pairs of sequence tags from the population;

c) selecting a pair of sequence tags from the population;

d) comparing each sequence tag of the selected pair with each sequence tag of a first pair and a last pair of a candidate ordering;

e) adding the selected pair to an end of the candidate ordering whenever a sequence tag of the selected pair matches the sequence tag of the first pair or the last pair of the candidate ordering, to form a new candidate ordering; and

f) repeating steps c) through e) until all pairs of the population have been selected.

24. (Withdrawn) The method of claim 23, wherein each population of pairs of sequence tags consists of n pluralities of pairs of sequence tags, each plurality being formed by digesting said fragment of genomic DNA in n separate reactions, each with a different n-1 combination of restriction endonucleases, wherein each pair of sequence tags is formed by ligating a portion of each end of each restriction fragment together.

25. (Withdrawn) The method of claim 24, wherein said population of pairs of sequence tags consists of samples of pairs of sequence tags from each of said n pluralities.

26. (Withdrawn) The method of claim 25, wherein each of said samples has the same size.

27. (Withdrawn) The method of claim 26, wherein n =3 and each said restriction

endonuclease has a six-basepair recognition site.

28. (Currently amended) A plurality of oligonucleotides derived from restriction fragments of a polynucleotide,

each said oligonucleotide containing first and second end segments from opposite ends of one such restriction fragment, wherein

said first end segment consists of a first end sequence, having 5 to 12 basepairs, immediately adjacent to a cleaved restriction site,

said second end segment consists of a second end sequence, having 5 to 12 basepairs, immediately adjacent to a cleaved restriction site,

and said first end sequence and said second end sequence[[s]] are ligated directly together;

wherein each end sequence contains the same number of basepairs;

and wherein each end sequence in the plurality of oligonucleotides is unique.

29. (Previously presented) The oligonucleotide composition of claim 28, wherein each said restriction fragment has ends produced by digestion with different restriction endonucleases.

30. (Previously presented) The oligonucleotide composition of claim 29, wherein each said restriction fragment has ends produced by digestion of two different restriction endonucleases selected from a group consisting of three different restriction endonucleases.

31. (Previously presented) The oligonucleotide composition of claim 30, wherein each of said three different restriction endonucleases has a six-basepair recognition site.

32-33. (Cancelled)